



THE UNIVERSITY *of* EDINBURGH

Edinburgh Research Explorer

Optimal mass selection policies for schemes with overlapping generations and restricted inbreeding

Citation for published version:

Villanueva, B, Bijma, P & Woolliams, J 2000, 'Optimal mass selection policies for schemes with overlapping generations and restricted inbreeding', *Genetics Selection Evolution*, vol. 32, no. 4, pp. 339-355.

Link:

[Link to publication record in Edinburgh Research Explorer](#)

Document Version:

Publisher's PDF, also known as Version of record

Published In:

Genetics Selection Evolution

Publisher Rights Statement:

Copyright 2000 INRA, EDP Sciences

General rights

Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy

The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.



Optimal mass selection policies for schemes with overlapping generations and restricted inbreeding

Beatriz VILLANUEVA^{a,*}, Piter BIJMA^b, John A. WOOLLIAMS^c

^a Scottish Agricultural College, West Mains Road, Edinburgh, EH9 3JG,
Scotland, UK

^b Animal Breeding and Genetics Group, Wageningen Institute of Animal Sciences,
Wageningen Agricultural University, Wageningen, The Netherlands

^c Roslin Institute (Edinburgh), Roslin, Midlothian, EH25 9PS, Scotland, UK

(Received 22 October 1999; accepted 13 March 2000)

Abstract – Optimum breeding schemes for maximising the rate of genetic progress with a restriction on the rate of inbreeding (per year or per generation) are investigated for populations with overlapping generations undergoing mass selection. The optimisation is for the numbers of males and females to be selected and for their distribution over age classes. Expected rates of genetic progress (ΔG) are combined with expected rates of inbreeding (ΔF) in a linear objective function ($\Phi = \Delta G - \lambda \Delta F$) which is maximised. A simulated annealing algorithm is used to obtain the solutions. The restriction on inbreeding is achieved by increasing the number of parents and, in small schemes with severe restrictions, by increasing the generation interval. In the latter case the optimum strategy for obtaining the maximum genetic gain is far from truncation selection across age classes. In most situations, the optimum mating ratio is one but the differences in genetic gain obtained with different mating ratios are small. Optimisation of schemes when restricting the rate of inbreeding per generation leads to shorter generation intervals than optimisation when restricting the rate of inbreeding per year.

optimal selection / overlapping generations / restricted inbreeding / mass selection / genetic gain

Résumé – **Stratégies optimales de sélection individuelle en générations chevauchantes et avec une contrainte sur l'augmentation de la consanguinité.** On a recherché les schémas de sélection optimaux pour maximiser le gain génétique tout en restreignant l'augmentation de la consanguinité (par an ou par génération) dans des populations sous sélection individuelle et à générations chevauchantes. L'optimisation concerne le nombre de mâles et de femelles à sélectionner et leurs distributions dans les différentes classes d'âge. Le progrès génétique espéré (ΔG) et l'augmentation attendue de la consanguinité (ΔF) sont combinés linéairement pour constituer l'objectif à maximiser ($\Phi = \Delta G - \lambda \Delta F$). Les solutions ont été obtenues

* Correspondence and reprints
E-mail: b.villanueva@ed.sac.ac.uk

à l'aide d'un algorithme simulé «en anneau». On a satisfait à la restriction sur la consanguinité en augmentant le nombre de parents et, dans les schémas de petite taille et avec une contrainte sévère, en augmentant l'intervalle de génération. Dans ce dernier cas, la stratégie optimale de sélection pour un gain génétique maximum se situait loin de la troncation à travers toutes les classes d'âge. Dans la plupart des situations, la valeur de d (nombre de femelles reproductrices par mâle sélectionné) optimale était égale à 1, mais le gain génétique est demeuré voisin de son maximum pour les valeurs de d proches de 1. Conduite en considérant l'augmentation de la consanguinité par génération, l'optimisation des schémas de sélection s'accompagnait d'un intervalle de génération plus court que lorsque la contrainte portait sur l'augmentation annuelle de la consanguinité.

sélection optimale / générations chevauchantes / contrainte sur la consanguinité / sélection individuelle / progrès génétique

1. INTRODUCTION

Recent studies on optimisation of selection policies in breeding programmes have focused on maximisation of genetic progress while restricting the accumulation of inbreeding. The restriction on inbreeding ensures maintenance of long-term response by constraining the reduction in genetic variance and it limits reduction in performance in traits showing inbreeding depression.

Optimal selection decisions with restricted inbreeding have been described for populations with discrete generations where individuals born at different times do not breed with one another [4,7,15,21,22,28]. However, in most populations there is a continuous range of ages, and individuals of different ages can breed together (*i.e.* generations overlap).

When generations overlap, selection is usually performed by truncation across age classes and the individuals selected are those with estimated breeding values above a given threshold [6]. If genetic progress is being achieved in the population then younger parents are expected to have higher breeding values and a higher proportion of them is expected to be selected [1]. Truncation across age classes has been described as the optimal strategy for maximising genetic gain in the short-term [1,11]. However, if restrictions on inbreeding are imposed, the optimal age distribution may depart from that obtained when ignoring inbreeding in the optimisation.

Dynamic procedures have been proposed recently for maximising genetic response while constraining the absolute increase of the inbreeding coefficient [16] or the rate of inbreeding [8] in schemes with overlapping generations. These studies are based on stochastic simulations of specific breeding schemes and provide useful guidance for day-to-day selection decisions in practice that involve a particular set of candidates for selection. However, they do not give a general insight into which are, *a priori*, the optimum schemes for maximising gain given the basic design variables (available resources, trait selected and restriction on inbreeding).

A priori optimisation of breeding programmes requires accurate predictions of rates of genetic gain and inbreeding [21,22]. For selected populations with overlapping generations, predictions of response have been available

for many years [10]. However, accurate predictions of rates of inbreeding accounting for the inheritance of selective advantage have been only developed recently [2, 25, 26].

This study extends the procedures developed for optimising the design of breeding programmes with discrete generations [21, 22] to the situation where generations overlap. Optimum designs for maximising gain with a restriction on the rate of inbreeding are obtained for populations under mass selection with overlapping generations. Restrictions on the rate of inbreeding per year and per generation were both considered. The optimisation is for the number of parents and their distribution across age classes. The optimisation procedure involves maximising a single objective function that combines predictions for rates of response and inbreeding.

2. METHODS

2.1. Population model

A population with overlapping generations under mass selection was modelled. The population model was described in detail by Bijma and Woolliams [3]. Briefly, there were up to c_{\max} age classes leading to a total of $2c_{\max}$ sex by age categories. Categories from 1 to c_{\max} correspond to males and categories from $1 + c_{\max}$ to $2c_{\max}$ correspond to females. The time between two selection rounds was taken to be one year. The age distribution of parents was kept constant across years. Each year the n_j individuals with the highest phenotypic values were selected from the j th category to produce the next generation. The ranking of individuals within categories was constant over time. The numbers selected from each category (n_j) were optimised as described later. Mating of selected individuals was at random and followed a hierarchical mating design in which each male was mated to d females. The mating ratio (d) was also optimised. Resources were constrained by keeping fixed the total number of offspring available for selection each year (T). The total numbers of males and females selected each year were $N_m = \sum_{j=1}^{c_{\max}} n_j$ and $N_f = \sum_{j=1+c_{\max}}^{2c_{\max}} n_j$, respectively. The number of offspring born per female (n_o) was determined by T and the total number of females selected; *i.e.* $n_o = T/N_f$. Equal numbers of male and female offspring available for selection were produced.

2.2. Rate of genetic gain

Predictions of rates of genetic progress were based on the theory of long-term genetic contributions and assumed the infinitesimal model [3, 23, 24, 26, 27]. These predictions account for changes in genetic parameters due to selection (Bulmer effect) but not for changes due to inbreeding. The expected value for the asymptotic rate of response (ΔG) is

$$E[\Delta G] = \sum_{j=1}^{2c_{\max}} n_j E[u_j a_j]$$

where u_j is the expected long-term contribution from an ancestor in category j and a_j is its Mendelian sampling term [26]. The expected long term genetic contribution for an ancestor i in category j is given by $u_{i(j)} = \alpha_j + \beta_j(A_{i(j)} - \bar{A}_j)$, where α_j is the expected contribution of an average parent in category j and β_j is the regression of the contribution of an individual in category j on its breeding value ($A_{i(j)}$), expressed as a deviation from the mean breeding value of selected contemporaries in category j (\bar{A}_j). The solutions for α_j and β_j were obtained as described in Bijma and Woolliams [3].

Substituting the value of $u_{i(j)}$ into the equation for $E[\Delta G]$ gives

$$E[\Delta G] = (0.5)\sigma_{a_0}^2 \left[\sigma_p^{-1} \sum_{j=1}^{2c_{\max}} n_j \alpha_j i_j + \sum_{j=1}^{2c_{\max}} n_j \beta_j (1 - k_j h^2) \right]$$

where i_j is the selection intensity in category j , k_j is the Pearson's variance reduction coefficient, $\sigma_{a_0}^2$ is the additive genetic variance in the unselected base population, and σ_p^2 and h^2 are the asymptotic (Bulmer equilibrium) phenotypic variance and heritability, respectively [3].

2.3. Rate of inbreeding and generation interval

The expected value for the asymptotic rate of inbreeding per year (ΔF_Y) is

$$E[\Delta F_Y] = (1/2) \sum_{s=1}^{c_{\text{exc}}} n_s E[u_s^2] + (1/8) \sum_{s=1}^{c_{\text{exc}}} n_s \delta_s$$

where subscript s represents exclusive categories, c_{exc} is the number of exclusive categories and δ is a correction factor for deviations of the variance of family size from independent Poisson variances [2, 25]. Derivations of $E[u_s^2]$ and δ_s are given in Bijma *et al.* [2] (equations 9 to 15) and a numerical example is described in their Appendix B.

The rate of inbreeding per generation (ΔF_G) was approximated by $\Delta F_G \approx L \Delta F_Y$, where L is the generation interval (in years) defined as the time in which genetic contributions sum to unity and given by $L = 1 / \sum_{j=1}^{2c_{\max}} n_j \alpha_j$ [3].

2.4. Optimisation of breeding schemes

The objective was to find the combination of numbers of individuals selected in each category that gives the highest annual rate of genetic gain for a pre-defined rate of inbreeding (per year or per generation). Thus the optimisation was for the set of n_j ($j = 1, \dots, 2c_{\max}$) and therefore implicitly for L and d . The predictions for ΔG and ΔF were combined in a single objective function, $\Phi = \Delta G - \lambda \Delta F$, which was maximised. The parameter λ is a Lagrangian multiplier that was increased until the desired ΔF was achieved [22]. From the theory of Lagrangian multipliers, maximisation of Φ is equivalent to maximising

ΔG with a constraint on ΔF . Both restrictions on ΔF_Y and on ΔF_G were investigated. The set of values for n_j ($j = 1, \dots, 2c_{\max}$) giving the maximum value for Φ was considered to be the optimum.

A minimum number of males to be selected was imposed in the optimisation to avoid inaccurate predictions of ΔG and ΔF which occur with extreme selection intensities [2]. The minimum N_m (N_{m_min}) depended on T (smaller values of T allow lower N_{m_min} for accurate predictions). The number of females to be selected was thus also constrained to dN_{m_min} . It should be noted however that the optimum numbers selected presented later were always higher than the minimum numbers allowed in the optimisation.

The optimisation was carried out in two steps. Firstly, optimum values for n_j ($j = 1, \dots, 2c_{\max}$) were obtained for fixed mating ratios (only integer values for d were allowed). Subsequently, the values of Φ obtained for schemes with the optimal age structure for different mating ratios were compared and the scheme giving the highest value of Φ was defined as the optimum (*i.e.* d was optimised in this second step).

For a given d the potential number of alternative schemes (*i.e.* number of possible combinations of numbers of individuals selected across categories) is very large. For instance, for $T = 200$, $d = 1$ and $c_{\max} = 5$ the number of possible combinations of males selected across age classes is $101^5 - 1$. Simultaneous optimisation of females leads to a very large-scale problem. The method of simulated annealing [18] is useful for this type of large optimisation combinatorial problem, where the objective function has many local maxima, and it was the method chosen for finding the optimal age structure for a given mating ratio. Although the method does not guarantee to find the global maximum it generally finds a solution close to the optimum that is very unlikely to be improved [17].

A summary of the steps carried out for the global optimisation is as follows:

1. Choose an initial value for λ (*e.g.* $\lambda = 0$).
2. Set the mating ratio (d) to 1.
3. Find the optimum n_j for each category (*i.e.* find the optimum \mathbf{n} , where $\mathbf{n}^T = (n_1 n_2 \dots n_{2c_{\max}})$) using simulating annealing (see later). Store the optimum \mathbf{n} (*i.e.* the \mathbf{n} giving the highest value of Φ for the given d) and corresponding Φ value.
4. Increase d by 1.
5. If d is less than or equal to its maximum possible value (*i.e.* $T/2N_{m_min}$) then go to step 3. If $d > T/2N_{m_min}$ then go to step 6.
6. Find the optimum d by comparing the Φ values obtained in step 3 with optimal \mathbf{n} for different d .
7. If $\Delta F =$ desired value: Stop.
8. If $\Delta F <$ desired value: Decrease λ and go to step 2.
9. If $\Delta F >$ desired value: Increase λ and go to step 2.

2.5. Simulated annealing algorithm

As mentioned above, the optimum numbers selected from each sex by age class were obtained for fixed values of λ and d using a simulated annealing

algorithm [18]. The optimal solution was that which minimised the objective function $-\Phi$. (Note that minimisation of $-\Phi$ gives the same solution as maximisation of Φ .) The steps involved in the algorithm were:

1. Generate at random an initial solution (*i.e.* an initial set of numbers selected for each category). Compute Φ for the initial solution.
2. Apply a small modification (the modifications considered are described below) to the current solution and compute Φ for the new solution.
3. If the modification decreases the objective function value then it is accepted and replaces the current solution. Otherwise, the modification is accepted with a probability $P = \exp(-\Delta\Phi/t)$, where $\Delta\Phi$ is the change in the objective function value (as a result of the modification) and t is the imaginary temperature (a control parameter in the annealing algorithm).
4. Decrease the value of t (*i.e.* multiply t by t_{fac} where $0 < t_{\text{fac}} < 1$) after x_{mod} modifications or after x_{suc} accepted modifications ($x_{\text{suc}} < x_{\text{mod}}$), whichever comes first. Both x_{mod} and x_{suc} are integers.
5. The optimal solution is found when the solution is unchanged during x_{mod} suggested modifications (*i.e.* steps 2 to 4 are repeated until x_{mod} successive modifications of the solution are not accepted).

The initial value of t and the values of t_{fac} , x_{mod} , and x_{suc} depended on the scored population size, the heritability and c_{max} . The initial t was set to a value considerably larger than the largest $\Delta\Phi$ encountered. Some trial and error was needed to find the values for t_{fac} , x_{mod} , and x_{suc} that led consistently to the optimal solutions.

The modifications to the current solution were chosen at random from the following five:

1. The number of males selected in category j (where j was chosen at random) was increased by one. Then the number of females selected was increased by the number needed to get the given integer mating ratio (d). The extra females selected were allocated at random across categories.
2. The number of males selected in category j (where j was chosen at random) was decreased by one. Then the number of females selected was decreased by the number needed to get the given d . The categories from which the selected male and females were removed were chosen at random.
3. The number of males selected was increased by one in category i and decreased by one in category j . Both categories were chosen at random.
4. The number of females selected was increased by one in category i and decreased by one in category j . Both categories were chosen at random.
5. The number of males selected was increased by one in category i and decreased by one in category j . Similarly the number of females selected was increased by one in category k and decreased by one in category l . Categories i , j , k and l were chosen at random.

Modifications 3, 4 and 5 imply no changes in the numbers selected.

Table I. Optimum numbers selected across categories for maximising the annual rate of gain under different restrictions on the annual rate of inbreeding (ΔF_Y), heritabilities (h^2) and scored population sizes (T) when two age classes are considered.

h^2	T	$\Delta F_Y \leq 1\%$				$\Delta F_Y \leq 0.5\%$				$\Delta F_Y \leq 0.25\%$			
		n_1^\dagger	n_2	n_3	n_4	n_1	n_2	n_3	n_4	n_1	n_2	n_3	n_4
0.1	50	3	10	3	10	2	12	0	14	1	18	0	19
	200	27	1	27	1	42	9	42	9	58	30	58	30
	800	36	0	36	0	63	1	63	1	107	5	107	5
	3 200	44	0	44	0	80	0	80	0	143	1	143	1
0.6	50	11	2	0	13	1	14	0	15	2	20	0	22
	200	32	1	32	1	48	13	48	13	36	57	36	57
	800	31	0	61	1	76	1	76	1	127	1	127	1
	3 200	39	0	78	0	69	0	137	1	126	0	251	1

† Categories 1 and 2 correspond to males and categories 3 and 4 correspond to females.

Table II. Annual rates of genetic gain (ΔG) and generation intervals (L) for optimal schemes under different restrictions on the annual rate of inbreeding (ΔF_Y), heritabilities (h^2) and scored population sizes (T) when two age classes are considered.

h^2	T	$\Delta F_Y \leq 1\%$		$\Delta F_Y \leq 0.5\%$		$\Delta F_Y \leq 0.25\%$	
		ΔG	L	ΔG	L	ΔG	L
0.1	50	0.059	1.745	0.040	1.922	0.023	1.972
	200	0.114	1.037	0.086	1.176	0.059	1.339
	800	0.166	1.000	0.142	1.016	0.115	1.045
	3 200	0.211	1.000	0.191	1.000	0.168	1.007
0.6	50	0.272	1.586	0.182	1.947	0.097	1.942
	200	0.533	1.036	0.395	1.211	0.260	1.542
	800	0.789	1.007	0.669	1.015	0.537	1.011
	3 200	1.012	1.000	0.910	1.003	0.789	1.002

3. RESULTS

3.1. Optimum schemes when restricting ΔF_Y for $c_{\max} = 2$

Table I shows the optimum numbers of males and females to be selected for obtaining the maximum ΔG under different constraints on ΔF_Y when the maximum number of age classes is 2. The corresponding gains and generation intervals resulting from the optimisation are shown in Table II. In all cases, the total numbers selected were larger than the minimum values allowed (*i.e.* $(n_1 + n_2) > N_{m_min}$ and $(n_3 + n_4) > dN_{m_min}$). For the cases studied, the optimum total numbers selected increased with the scored population size, the

heritability and the severity in restricting ΔF_Y . The optimum mating ratio was one (*i.e.* $N_m = N_f$) except for a high heritability and the larger schemes. In these cases the optimum d increased to 2. For the least severe restriction on inbreeding considered ($\Delta F_Y \leq 1\%$), the maximum gain was obtained by selecting the youngest individuals unless the schemes were very small ($T = 50$). For $T \geq 200$ the optimum L was very close to one in all cases when restricting ΔF_Y to 1%.

More severe restrictions on ΔF_Y were achieved by decreasing the intensity of selection (*i.e.* by increasing N_m and N_f) and, in the smaller schemes, by selecting older individuals. The optimal L increased by up to 23% and 17% ($h^2 = 0.6$) with $T = 50$ and 200, respectively, when the restriction on ΔF_Y was changed from 1% to 0.5%. With $h^2 = 0.6$ and the most severe restriction considered ($\Delta F_Y \leq 0.25\%$), L increased by up to 22% and 49% (relative to $\Delta F_Y \leq 1\%$) with $T = 50$ and 200, respectively. The increase in L found when imposing more severe restrictions on inbreeding was less acute with the largest schemes; only small increases in L were observed in schemes of size $T = 800$ and the optimum L remained practically unchanged ($L = 1$) in the largest schemes ($T = 3200$) across heritabilities and restrictions on ΔF_Y .

The rate of genetic progress increased with the scored population size and the heritability and decreased with the severity in the restriction on ΔF_Y . The loss in gain by restricting ΔF_Y to 0.5% relative to the gain obtained when $\Delta F_Y \leq 1\%$ ranged from 10% ($T = 3200$, $h^2 = 0.6$) to 32% ($T = 50$, $h^2 = 0.1$). In percentage, the decrease in ΔG was approximately doubled when restricting ΔF_Y to 0.25% (relative to the gain obtained when $\Delta F_Y \leq 1\%$).

3.2. Optimum schemes when restricting ΔF_Y for fixed d and $c_{\max} = 4$

Table III shows optimal age structures and rates of progress when fixing d to specific values (1 to 4). The annual rate of inbreeding was restricted to 1% and the maximum number of age classes was four. For a given restriction on inbreeding ($\Delta F_Y \leq 1\%$ in this case), the differences in gain with different mating ratios were small. The loss in gain when fixing d to 4 relative to the gain obtained with the optimum d ($d = 1$ or 2, depending on h^2 and T) ranged from 3% ($T = 800$, $h^2 = 0.6$) to 7% ($T = 200$, $h^2 = 0.1$) for the cases considered.

As d increases fewer and younger males and more and older females need to be selected to achieve the maximum gain under constrained ΔF_Y . The increase in L with d was small and it was a consequence of selecting more females in older categories.

3.3. Restriction on ΔF_Y versus restriction on ΔF_G

Optimum schemes presented above were obtained when imposing a constraint on the annual rate of inbreeding (ΔF_Y). The optimum generation interval differed from one, particularly when the schemes were small. Table IV shows a comparison of optimum schemes when imposing a constraint on ΔF_Y versus optimum schemes when imposing a constraint on the rate of inbreeding

Table III. Effect of mating ratio (d) on the annual rate of gain (ΔG) and the generation interval (L) when the annual rate of inbreeding is restricted to 1% for different scored population sizes (T) and heritabilities (h^2). The numbers selected across categories (n_j , $j = 1, \dots, 8$) were optimised for maximising ΔG for fixed d . The number of age classes was 4.

h^2	T	d	ΔG	L	n_1^\dagger	n_2	n_3	n_4	n_5	n_6	n_7	n_8
0.1	200	1	0.114	1.037	27	1	0	0	27	1	0	0
		2	0.113	1.109	19	1	0	0	34	5	1	0
		3	0.109	1.122	17	0	0	0	39	11	1	0
		4	0.106	1.179	15	0	0	0	42	14	3	1
	800	1	0.166	1.000	36	0	0	0	36	0	0	0
		2	0.165	1.009	26	0	0	0	51	1	0	0
		3	0.162	1.014	22	0	0	0	64	2	0	0
		4	0.159	1.023	20	0	0	0	76	4	0	0
	0.6	1	0.533	1.036	32	1	0	0	32	1	0	0
		2	0.524	1.085	24	0	0	0	40	7	1	0
		3	0.515	1.110	20	0	0	0	46	13	1	0
		4	0.514	1.140	17	0	0	0	48	17	3	0
	800	1	0.785	1.000	45	0	0	0	45	0	0	0
		2	0.789	1.007	31	0	0	0	61	1	0	0
		3	0.779	1.006	26	0	0	0	77	1	0	0
		4	0.763	1.017	24	0	0	0	92	4	0	0

\dagger Categories 1 to 4 correspond to males and categories 5 to 8 correspond to females.

per generation (ΔF_G) for schemes of size $T = 50$ or $T = 200$ and $c_{\max} = 2$. For a particular combination of heritability and restriction on ΔF_Y , the rate of inbreeding per generation was restricted to the value obtained for ΔF_G in the scheme restricting ΔF_Y . For instance, for $h^2 = 0.1$, $T = 50$ and the restriction $\Delta F_Y \leq 1\%$, the value obtained for ΔF_G was 1.74%. Thus the comparison was for the optimum scheme (with the same heritability and resources) obtained when imposing the constraint $\Delta F_Y \leq 1.00\%$ versus the optimum scheme obtained when imposing the constraint $\Delta F_G \leq 1.74\%$.

Imposing a constraint on ΔF_G rather than on ΔF_Y substantially reduced the optimum generation interval. Note that $\Delta F_G \approx L\Delta F_Y$ and therefore the restriction on ΔF_G can be achieved by decreasing L . Higher annual rates of response were obtained with the restriction on ΔF_G than with the restriction on ΔF_Y . However, this was a consequence of the order in which optimisations were performed. If the scheme had been first optimised with a constraint on ΔF_G and subsequently with a constraint on ΔF_Y , higher responses would have been obtained with the restriction on ΔF_Y . For instance, for $h^2 = 0.1$, $T = 200$, and the restriction $\Delta F_G \leq 0.59\%$, the optimal age distribution was $\mathbf{n}^T = (41 \ 1 \ 41 \ 1)$ and the values obtained for ΔG and ΔF_Y were 0.090 and 0.57%, respectively. A subsequent optimisation with a restriction on ΔF_Y ($\Delta F_Y \leq 0.57\%$) led to higher rate of gain ($\Delta G = 0.092$). The optimal distribution in the latter case was $\mathbf{n}^T = (39 \ 6 \ 39 \ 6)$.

Table IV. Optimum numbers selected across categories (n_1, n_2, n_3, n_4) for maximising the annual rate of gain (ΔG) when restricting the rate of inbreeding per year (ΔF_Y , in %) or per generation (ΔF_G , in %) for different heritabilities (h^2) and scored population sizes (T). The number of age classes was 2.

h^2	T	Restriction	ΔF_Y	ΔF_G	ΔG	n_1^\dagger	n_2	n_3	n_4	L
0.1	50	$\Delta F_Y \leq 1.00\%$	1.00	1.74	0.059	3	10	3	10	1.745
		$\Delta F_G \leq 1.74\%$	1.59	1.71	0.074	13	1	13	1	1.075
		$\Delta F_Y \leq 0.50\%$	0.50	0.96	0.040	2	12	0	14	1.922
		$\Delta F_G \leq 0.96\%$	0.89	0.94	0.045	19	1	19	1	1.053
	200	$\Delta F_Y \leq 0.50\%$	0.50	0.59	0.086	42	9	42	9	1.176
		$\Delta F_G \leq 0.59\%$	0.57	0.58	0.090	41	1	41	1	1.025
	0.6	$\Delta F_Y \leq 1.00\%$	0.99	1.57	0.272	11	2	0	13	1.586
		$\Delta F_G \leq 1.57\%$	1.40	1.56	0.317	12	0	19	5	1.113
		$\Delta F_Y \leq 0.50\%$	0.49	0.94	0.182	1	14	0	15	1.947
		$\Delta F_G \leq 0.94\%$	0.93	0.93	0.205	19	0	19	0	1.000
	200	$\Delta F_Y \leq 0.50\%$	0.49	0.60	0.395	48	13	48	13	1.211
		$\Delta F_G \leq 0.60\%$	0.59	0.59	0.423	45	0	45	0	1.000

\dagger Categories 1 and 2 correspond to males and categories 3 and 4 correspond to females

4. DISCUSSION

Recent developments in prediction of rates of inbreeding for selected populations with overlapping generations [2,25,26] allow deterministic optimisation of designs of breeding programmes under constrained inbreeding. In this study, optimum breeding designs giving the maximum rate of genetic progress while restricting the rate of inbreeding (per year or per generation) have been described for populations undergoing mass selection. The optimisation procedure used was an extension to that developed for populations with discrete generations [22]. With overlapping generations, the restrictions on inbreeding were mostly achieved by increasing the numbers of parents selected and to a lesser extent by increasing the generation interval. In most cases, the optimum schemes under restricted inbreeding were those selecting equal number of males and females although the differences in gain for different mating ratios were small.

The optimal strategy for obtaining the maximum gain while restricting the rate of inbreeding to a particular value depends on the relationships among the rates of gain and inbreeding, the number of parents selected and the distribution of parents over age classes. An example of these relationships is given in Figure 1 for $T = 100$ or 400 and $h^2 = 0.3$ and a maximum of two age classes. Both the rate of gain and the rate of inbreeding decrease with the total number of parents selected but the proportional reduction in the rate of inbreeding is

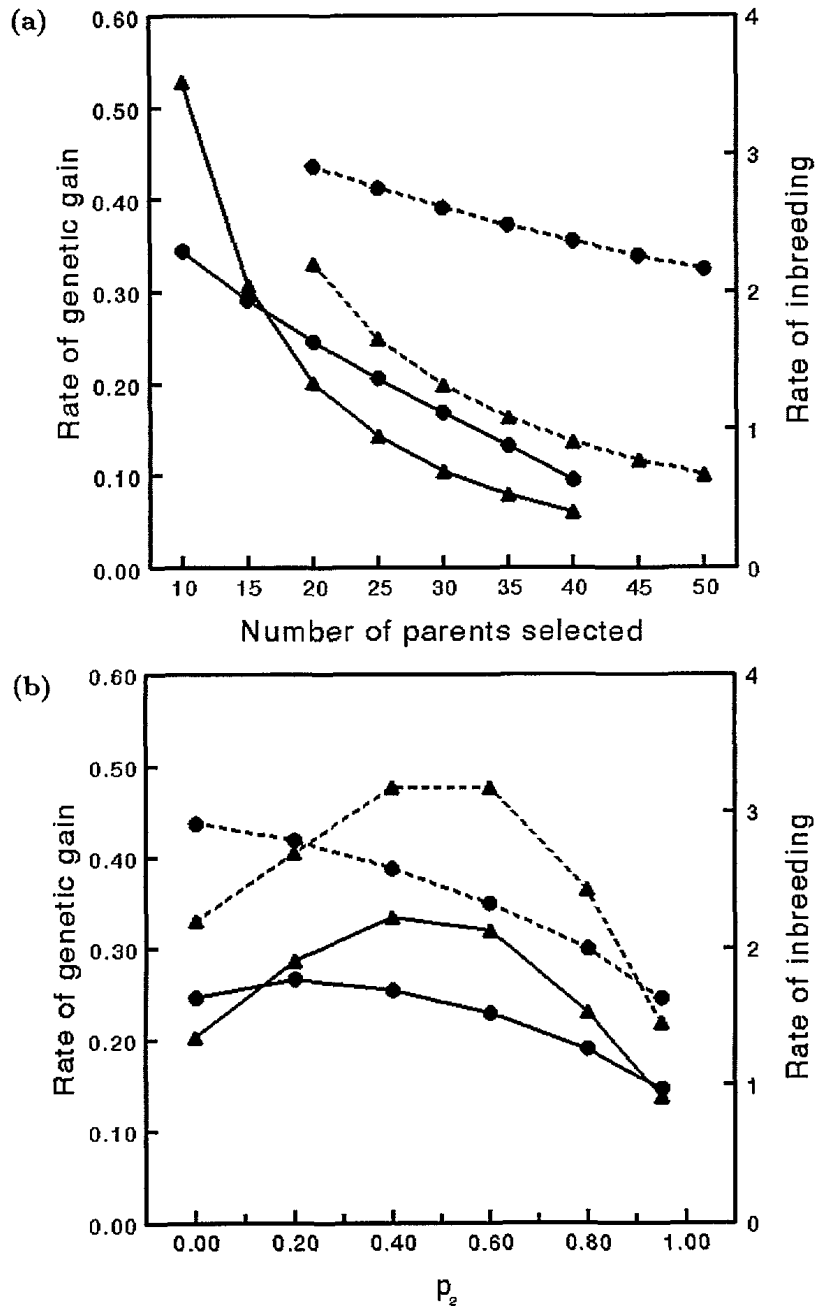


Figure 1. Annual rate of genetic gain, in σ_p units, (\bullet) and rate of inbreeding per generation, in %, (\blacktriangle) for (a) different numbers of parents selected and $c_{\max} = 1$ and (b) different proportions of parents in the second age class (p_2) when the number of parents selected of each sex is 20 and $c_{\max} = 2$. The heritability was 0.3, the mating ratio was one and the number of offspring born per year was 100 (solid line) or 400 (dotted line).

higher than the reduction in gain (Fig. 1a). Doubling the number of parents when keeping T constant more than halves the rate of inbreeding (as would be the case if ΔF is predicted by using $(1/8N_m) + (1/8N_f)$). With selection, the rate of inbreeding is a function of approximately i^2/N_m and i^2/N_f (equation 7 of Bijma *et al.* [2]) and these terms decrease faster than $1/N_m$ and $1/N_f$ when decreasing the intensity of selection.

The relationships among the rates of gain and inbreeding and the distribution of parents over age classes are more complex (Fig. 1b). In general, the rate of gain decreases as the proportion of parents in the oldest class increases. However, the rate of inbreeding reaches a maximum when the parents are equally distributed across classes (the same individuals are selected in consecutive years) and a minimum when most parents are in the oldest class (more parents enter the population each generation) [2]. These relationships lead to the fact that the restriction on inbreeding per generation with mass selection is mainly achieved by selecting more parents. For example, by increasing the number of parents of each sex (N_m and N_f) from 20 to 25, the rates of gain and inbreeding are reduced respectively by 16% and 29% for $T = 100$ and by 6% and 24% for $T = 400$. However, for $N_m = N_f = 20$, the increase in the proportion of parents in the oldest class from 0% to 95% reduced the rates of gain and inbreeding respectively by 41% and 32% for $T = 100$ and by 44% and 34% for $T = 400$. Thus, less gain is lost by selecting more parents than by increasing the generation interval when restrictions on inbreeding are imposed.

With no control on the accumulation of inbreeding, the optimal strategy for maximising gain in populations with overlapping generations is to select the individuals with the highest genetic merit independently of their age; *i.e.* truncation selection across age classes [1,6]. If there is any genetic trend in the population, this strategy implies that most parents selected would belong to the youngest age class (one-year-old in this study). This study shows that when the rate of inbreeding is restricted then truncation selection across age classes may not be the optimum strategy for maximising gain. As mentioned above, in some situations, the imposition of restrictions on the rate of inbreeding led not only to an increased total number of parents but also to an increased number of individuals selected from older age classes. In some situations, particularly with small schemes or with severe restrictions and high heritability, the optimal strategy was far from truncation selection across age classes and that was due to the restriction on inbreeding. For instance for $T = 50$, $h^2 = 0.1$, $\Delta F_Y \leq 1\%$ and $c_{\max} = 2$, the optimal age distribution was $\mathbf{n}^T = (3 \ 10 \ 3 \ 10)$ (Tab. I) whereas without any restriction on inbreeding and the same number of parents selected ($N_m = N_f = 13$) the optimal distribution was $\mathbf{n}^T = (10 \ 3 \ 10 \ 3)$. With $\mathbf{n}^T = (10 \ 3 \ 10 \ 3)$ the annual rate of inbreeding was 1.93%.

In most situations the maximum gain was achieved when the selection proportions were the same in both sexes (*i.e.* optimum $d = 1$). Only when the heritability was high and the size of the scheme was large the optimum d increased to 2. By imposing more stringent constraints on inbreeding in these schemes the optimum d changed to 1 (Tab. I). These results were also found for populations with discrete generations by Villanueva *et al.* [22] who related the

deviation from 1 of the optimum d observed in some cases, to the prediction of the rate of inbreeding in schemes with hierarchical matings. Complete factorial mating designs may lead to maximum gains with $d = 1$ across heritabilities and scheme sizes.

Full exploitation of resources can be difficult to achieve in practice with optimal mating ratios ($d \leq 2$), particularly in animal populations where the reproductive capacity of males is often much larger than in females. Results from this study (Tab. III) show that little genetic gain was lost by using higher mating ratios with restricted rate of inbreeding. The decrease in the selection intensity in females as a result of imposing values for d higher than the optimum (*i.e.* more females needed to be selected) was in part compensated for an increase in the selection intensity in males. The net result was a small reduction in the rate of genetic progress.

The study has assumed unlimited reproductive capacities (*i.e.* the number of offspring per breeding animal is unlimited). In practice, this may be appropriated for fish breeding schemes but also for livestock schemes using advanced reproductive techniques (*e.g.* *in vitro* production of embryos). However, limitations on the number of offspring a female may produce are likely to occur in practice. This situation could be accommodated into the optimisation simply by increasing the minimum number of breeding females (dN_{m_min}) allowed in the procedure. The study also assumes that the first progeny can be obtained at one year of age. For species where this is not possible, the procedure could also be easily modified to allow higher minimum ages at breeding. The constraints on limited reproductive capacity and minimum age for breeding would result in lower gains to those presented here.

Optimum schemes have been presented for maximising the annual rate of gain while restricting the rate of inbreeding per year (ΔF_Y) or per generation (ΔF_G). Whereas, in practice, maximisation of gain on an annual basis is clearly the choice, the appropriateness of restricting the rate of inbreeding per year or per generation is less clear. Our results show that unless the constraint on inbreeding is very severe and the schemes are of small size, the optimal generation interval is close to one and therefore, in most situations, there is no argument about restricting ΔF_G or ΔF_Y .

However, with small schemes such as those involved in conservation programmes and with a restriction on the annual rate of inbreeding, the optimal generation interval was far from one. Also, the generation interval can deviate from one if the trait can not be measured before the individuals are one year old. When schemes were compared at a fixed ΔF_G , the restriction on ΔF_G led to shorter generation intervals than the restriction on ΔF_Y . Similar results have been found by Sonesson *et al.* [20]. If the accumulation of mutational variance occurs on a per generation basis and it is of interest to safeguard the existence of the population, then restricting ΔF_G may be the appropriate choice since shorter generation intervals would imply higher genetic variability for a fixed period of time. However, there may be situations where, to satisfy particular customers, breeding companies (*e.g.* pig or poultry companies) may be prepared to take the risk of losing some lines. In the latter situation the interest is short-term optimisation and the aim may be to maximise gain over a fixed time horizon. Also, there

could be an argument to increase the generation interval for traits exhibiting inbreeding depression since depression is proportional to the level of inbreeding and then it would increase faster in a scheme with restrictions on ΔF_G .

When selection is based only on the individual performance of the candidates (*i.e.* mass selection), the accuracy of selection is the same across age classes. In practice, most breeding programmes make use of performance information of relatives, including descendants, and therefore the selection criterion may vary across age classes. For instance, with BLUP selection, the estimates of breeding values of older individuals are expected to be more accurate than for those for younger individuals since EBVs of older individuals are based on more information. In schemes with no progeny testing, optimal generation intervals with mass and BLUP selection may however be similar. On the one hand, the rate of genetic gain is expected to be higher with BLUP and this gives younger individuals an increased selective advantage. But on the other hand, BLUP is also expected to give a higher rate of inbreeding and then for a specific restriction on the inbreeding rate, BLUP may favour more parents from the older age classes to be selected.

Two recent studies [8,16] have investigated optimal generation intervals for schemes with overlapping generations using BLUP estimates as a predictor of genetic merit. Meuwissen and Sonesson [16] found large increases in L in schemes with progeny testing in comparison to schemes with no progeny testing. With progeny testing, there is a lower intraclass correlation between EBVs of sibs. Therefore, selection of progeny tested individuals will give more gain at a fixed rate of inbreeding. However, the restrictions they applied were on the annual rate of inbreeding, which leads to longer generation intervals than restrictions per generation.

The methods of Meuwissen and Sonesson [16] and Grundy *et al.* [8] are aimed to maximise progress with constraints on rates of inbreeding in the routine operation of breeding schemes (day-to-day optimisation). This is a different type of optimisation to the one we deal with in this study. Here the optimisation is *a priori*, to maximise gain given the basic design variables (available resources, trait selected and restriction on inbreeding). In this situation, the ability to solve the problem depends on appropriate models for predicting both rates of gain and inbreeding and on appropriate algorithms for obtaining optimum solutions which maximise the objective function ($\Phi = \Delta G - \lambda \Delta F$). Appropriate approaches for obtaining predictions of inbreeding with overlapping generations have been described for index selection (including the index approximating BLUP) [25,26] but explicit formulae need to be developed. With more variables to be optimised (*e.g.* index weights) with index selection, the computer time required for finding the optimal solutions could be prohibitively large for schemes with overlapping generations when using simulated annealing algorithms (the number of evaluations of Φ is already very large with mass selection). Genetic algorithms [9,14,19] may prove to be useful in this situation.

Predictions for the rates of progress and inbreeding used in the optimisation have assumed a population with equilibrium genetic parameters. With constant selection intensities across generations, the rate of inbreeding reaches

an equilibrium value after an appropriate number of generations. However, the rate of progress would steadily decrease with time as a result of the decrease in genetic variance. Here we have considered the rate of progress at Bulmer equilibrium, thus ignoring further decreases in genetic variability in later generations due to inbreeding. Villanueva and Woolliams [21] found that under restricted inbreeding, the optimum schemes for maximising gain at different time horizons were very similar when the changes in genetic variance due to inbreeding were accounted for in populations with discrete generations. This could also be expected when generations overlap since by restricting the rate of inbreeding the loss of genetic variance is also restricted.

The highest optimal generation intervals (L) were found for the smallest schemes and the most stringent restrictions on ΔF_Y . For $T = 50$, $h^2 = 0.6$ and $\Delta F_Y \leq 0.25$, the optimal L was 1.94 (and $N_m = N_f = 22$). Let us consider twenty years of selection which is equivalent to 20 or 10 generations for $L = 1$ or $L = 1.94$, respectively. With discrete generations and accounting for the reduction in genetic variance due to inbreeding, the cumulative gain was 0.0802 and 0.0836 after 20 and 10 generations, respectively. Thus even with small schemes of size 50, the reduction in gain is not very large when the rate of inbreeding and therefore the loss of genetic variability are constrained.

In addition, in practice there will be new genetic variation produced by mutation. If the only processes involved in the evolution of the genetic variance are mutation and random drift then the population will eventually approach an equilibrium where the loss in variance due to random drift will be balanced by the new variation by mutation [13]. At equilibrium and on a generation basis, the genetic variance can be approximated by $\sigma_m^2/\Delta F_G$ where σ_m^2 is the mutational variance [13] and therefore the equilibrium value for the heritability is $h_{eq}^2 = (\sigma_m^2/\Delta F_G)/[(\sigma_m^2/\Delta F_G) + \sigma_e^2] = (\sigma_m^2/\sigma_e^2)/[(\sigma_m^2/\sigma_e^2) + \Delta F_G]$, where σ_e^2 is the environmental variance. A recent estimate of the mutational variance scaled by σ_e^2 for 6-week weight in the mouse is $\sigma_m^2/\sigma_e^2 = 0.0034$ [5, 13]. Assuming this value for σ_m^2/σ_e^2 and a restriction on ΔF_G of 1%, the equilibrium heritability is 0.25, which indicates that the mutation rate may be high enough to compensate for the loss of genetic variability due to inbreeding when $\Delta F_G \leq 1\%$. Less conservative estimates of the mutational variance (*e.g.* [12]) would lead to even higher values for the equilibrium heritability.

ACKNOWLEDGEMENTS

Part of this work was undertaken during a visit to the Wageningen Agricultural University by BV; SAC and the Wageningen Agricultural University are acknowledged for financial support. PB acknowledges financial support from the Netherlands Technology Foundation (STW). SAC receives financial support from the Scottish Executive Rural Affairs Department. Work at the Roslin Institute receives support from the Ministry of Agriculture, Fisheries and Food (UK).

REFERENCES

- [1] Richard M., Pease A.H.R., Swales P.H., Özkütük K., Selection in a population with overlapping generations, *Anim. Prod.* 17 (1973) 215–227.
- [2] Bijma P., van Arendonk J.A.M., Woolliams J.A., A general procedure for predicting rates of inbreeding in populations undergoing mass selection, *Genetics* 154 (2000) 1865–1877.
- [3] Bijma P., Woolliams J.A., Prediction of genetic contributions and generation intervals in populations with overlapping generations under selection, *Genetics* 151 (1999) 1197–1210.
- [4] Brisbane J.R., Gibson J.P., Balancing selection response and rate of inbreeding by including genetic relationships in selection decisions, *Theor. Appl. Genet.* 91 (1995) 421–431.
- [5] Caballero A., Keightley P.D., Hill W.G., Accumulation of mutations affecting body weight in inbred mouse lines, *Genet. Res.* 65 (1995) 145–149.
- [6] Ducrocq V., Quaas R.L., Prediction of genetic response to truncation selection across generations, *J. Dairy Sci.* 71 (1988) 2543–2553.
- [7] Grundy B., Villanueva B., Woolliams J.A., Dynamic selection procedures for constrained inbreeding and their consequences for pedigree development, *Genet. Res.* 72 (1998) 159–168.
- [8] Grundy B., Villanueva B., Woolliams J.A., Dynamic selection for maximising response with constrained inbreeding in schemes with overlapping generations, *Anim. Sci.* 70 (2000) 373–382.
- [9] Hayes B.J., Shepherd R.K., Newman S., Kinghorn B.P., A tactical approach to improving long term response in across breed mating plans, in: *Proceedings of the 6th World Congress on Genetics Applied to Livestock Production*, 11–16 January 1998, vol. 25, University of New England, Armidale, Australia, pp. 439–442.
- [10] Hill W.G., Prediction and evaluation of response to selection with overlapping generations, *Anim. Prod.* 18 (1974) 117–139.
- [11] James J.W., Determination of optimal selection policies, *J. Anim. Breed. Genet.* 104 (1987) 23–27.
- [12] Keightley P.D., Genetic basis of response to 50 generations of selection on body weight in inbred mice, *Genetics* 148 (1998) 1931–1939.
- [13] Lynch M., Walsh B., *Genetics and analysis of quantitative traits*, 1st edn., Sinauer Associates, Sunderland, 1998.
- [14] Meszaros S.A., Banks R.G., van der Werf J.H.J., Goddard M., The use of genetic algorithms for optimizing age structure in breeding populations when inbreeding depress genetic gain through effects of reproduction, *Anim. Sci.* 68 (1999) 449–457.
- [15] Meuwissen T.H.E., Maximizing the response of selection with a predefined rate of inbreeding, *J. Anim. Sci.* 75 (1997) 934–940.
- [16] Meuwissen T.H.E., Sonesson A.K., Maximizing the response of selection with a predefined rate of inbreeding: Overlapping generations, *J. Anim. Sci.* 76 (1998) 2575–2583.
- [17] Meuwissen T.H.E., Woolliams J.A., Maximizing genetic response in breeding schemes of dairy cattle with constraints on variance of response, *J. Dairy Sci.* 77 (1994) 1905–1916.
- [18] Press W.H., Teukolsky S.A., Vetterling W.T., Flannery B.P., *Numerical recipes in FORTRAN: the art of scientific computing*, 2nd edn., Cambridge University Press, Cambridge, 1992.

- [19] Shepherd R.K., Kinghorn B.P., A tactical approach to the design of crossbreeding programs, in: Proceedings of the 6th World Congress on Genetics Applied to Livestock Production, 11–16 January 1998, vol. 25, University of New England, Armidale, Australia, pp. 431–438.
- [20] Sonesson A.K., Grundy B., Woolliams J.A., Meuwissen T.H.E., Selection with control of inbreeding in populations with overlapping generations: a comparison of methods, *Anim. Sci.* 70 (2000) 1–8.
- [21] Villanueva B., Woolliams J.A., Optimization of breeding programmes under index selection and constrained inbreeding, *Genet. Res.* 69 (1997) 145–158.
- [22] Villanueva B., Woolliams J.A., Gjerde B., Optimum designs for breeding programmes under mass selection with an application in fish breeding, *Anim. Sci.* 63 (1996) 563–576.
- [23] Villanueva B., Woolliams J.A., Simm G., Evaluation of embryo sexing and cloning in dairy cattle nucleus schemes under restricted inbreeding, in: Proceedings of the 6th World Congress on Genetics Applied to Livestock Production, 11–16 January 1998, vol. 25, University of New England, Armidale, Australia, pp. 451–454.
- [24] Woolliams J.A., A recipe for the design of breeding schemes, in: Proceedings of the 6th World Congress on Genetics Applied to Livestock Production, 11–16 January 1998, vol. 25, University of New England, Armidale, Australia, pp. 427–430.
- [25] Woolliams J.A., Bijma P., Prediction of rates of inbreeding in selected populations, *Genetics* 154 (2000) 1851–1864.
- [26] Woolliams J.A., Bijma P., Villanueva B., Expected genetic contributions and its impact on gene flow and genetic gain, *Genetics* 153 (1999) 1009–1020.
- [27] Woolliams J.A., Thompson R., A theory of genetic contributions, in: Proceedings of the 5th World Congress on Genetics Applied to Livestock Production, 7–12 August 1994, vol. 19, University of Guelph, Guelph, Canada, pp. 127–133.
- [28] Wray N.R., Goddard M.E., Increasing long term response to selection, *Genet. Sel. Evol.* 26 (1994) 431–451.